

Figure 1: Stand alone Genome Threader results for INSP093 partial polypeptide sequence (SEQ ID NO:6).

Genome Threader results - Energy Scores

Num	EDB Clnt	Norm Align Score	Raw Align Score	%ID	%Struct Aligned	%Query Seq Aligned	Energy Score	Solvent Energy	Neutral Net Score	%Consistent	From Pos for Query	To Pos for Query	From Pos for Subject	To Pos for Subject	Alignment Length	Gap Length
1	1qg7 Haplosporin (Hsp)	30.58	53	25.0	78.8	44.7	10.39	-2.31	0.928	65	50	117	1	52	68	0
2	2ed1-10d Haplosporin (Hsp)	30.51	53	25.0	77.6	44.7	10.54	-2.10	0.927	65	50	117	2	53	68	0
3	1naa000 Haplosporin (Hsp)	28.52	60	13.4	17.2	63.8	8.64	2.81	0.597	54	47	143	36	128	97	0
4	2ed1-10d Haplosporin (Hsp)	21.04	57	10.9	14.5	35.5	-2.97	-0.08	0.893	53	97	150	78	132	59	0
5	2ed1-10d Haplosporin (Hsp)	26.47	60	45.2	2.6	18.4	-0.22	-2.31	0.896	54	107	134	603	625	31	0

Number 1: 1qg7, Stroma cell-derived factor-1alpha

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Figure 2: Alignment between INSP093 partial polypeptide sequence (SEQ ID NO:6) and the top hit, 1qg7.

```
1qg7BB00 -----PVSLSYRCPCR-----FF
                               :: : E E.
INSP093  msaqhglvskfglgllllgdkyfqrheqskphqeeidnlhspdlptpgHPVTLHSLCFCSPRGTLLEGPM
          10|      20|      30|      40|      50|      60|      70|

          20|      30|      40|      50|      60|
1qg7BB00  ESHVARANVKHLKILNTPN-----CALQI--VARLKNNNRQVCIDPklkwieylekaln-----
          ... .. : ... .. : .. : ... .. : ... .. :
INSP093  SSGFHRFEVENLRPQTAPKAGKGOMCGERMARMARTAKEGRPRCLDPglstrtphpgphvflphsptpasw
          80|      90|     100|     110|     120|     130|     140|

1qg7BB00 -----

INSP093  hqwapggtgwml
          150|
```

Highlighted residues identify the conservation of cysteines between 1qg7 and INSP093.

Figure 3: Stand alone Genome Threader results for INSP094 partial polypeptide sequence (SEQ ID NO:10).

Genome Threader results - Energy Scores

Num	PDB Code	Query Align Score	Raw Align Score	% ID	% Ident Aligned	% Ident Seq Aligned	Entropy Energy	Solvation Energy	Mineral Net Score	% Confidence	From Pos for Query	To Pos for Query	From Pos for Target	To Pos for Target	Alignment Length	Local-0 Global
1	1qzj:800 (align)	90.58	53	25.0	78.8	44.7	10.39	-2.31	0.928	65	50	117	1	52	68	0
2	Redt:100 (align)	90.51	53	25.0	77.6	44.7	10.54	-2.10	0.927	65	50	117	2	53	68	0
3	1pau:100 (align)	28.52	60	13.4	17.2	63.8	8.64	2.81	0.897	54	47	143	36	128	97	0
4	2511:100 (align)	27.04	57	10.9	14.5	35.5	2.37	-0.08	0.893	53	97	150	78	132	55	0
5	2511:100 (align)	26.47	60	45.2	2.6	18.4	-0.22	-2.31	0.896	54	107	134	603	625	31	0

Number 1: 1hum, *Homo sapiens* macrophage inflammatory protein

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Figure 4: Alignment between INSP094 partial polypeptide sequence (SEQ ID NO:10) and the top hit, 1hum.

```

1humAA00 -----apmgsdpptaCCFs
                               :
INSP094  ntendfyeicgnqshhhdnariKKlvdglefsqtmafsatkinmlfsqnhwtirsifhsgfywgkgCHK
              10|      20|      30|      40|      50|      60|      70|

              20|      30|      40|      50|      60|
1humAA00  YTAR-KLPRNFVVDYYETSSLCSQPAVVVFQTKRSKQV-CADPSESWVQEYvydleln
          . . . . . : : : : : : : : : : : : : : : : : :
INSP094  MSVHLFIHISN--RYFMTTSMQEMAKIL----GRQIKCYLPTQSPVRESggktif-
              80|      90|      100|      110|      120|

```

Highlighted residues identify the conservation of cysteines between 1hum and INSP094.

Figure 5: Nucleotide sequence of INSP094 with translation

```

1  cctggaacat aattgacatt caataaataa ctgttgaatt aatttgttga attaatgact
61  caagagtatt cacctttcat acataggaaa tagaatatag aataccgaga atgattttta
                                n t e n d f

121  tgagatctgt ggaaatcagt cacatcatca cgacaatgca agaataaaga agttagtaga
    y e i c  g n q  s h h  h d n a  r i k  k l v

181  tggccttgag ttttcccaa caatggcatt ttctgctacc aaaataaata tgttattcag
    d g l e  f s q  t m a  f s a t  k i n  m l f
                                INSP094-CP1 →

241  tcagaaccac tggactataa gaagtatatt ccattctggt ttttactggg ggaaaggatg
    s q n h  w t i  r s i  f h s g  f y w  g k g

301  ttgccacaag atgtcagtcc atttattcat tcatatatcc aatagatatt ttatgaccac
    c c h k  m s v  h l f  i h i s  n r y  f m t

361  ttccatgtgc caggagatgg ctaagatcct tggaagacag ataaaatgct acctaccaac
    t s m c  q e m  a k i  l g r q  i k c  y l p

421  tcaaagtcca gttagggagt cagggggtaa aacaatattc tagcacagtg tgttgaggcc
    t q s p  v r e  s g g  k t i f
                                ← INSP094-CP2

481  atggcatggt gagcacagga gcctgaagga gtggatggaa aaggcacctc agaatcatga
541  cactaggaaa tgattctcag t

```

Position and sense of PCR primers →

Figure 6: Nucleotide sequence with translation of PCR product cloned using primers INSP094-CP1 and INSP094-CP2

```

1  atggcatttt ctgctaccaa aataaatatg ttattcagtc agaaccactg gactataaga
   m a f s a t k i n m l f s q n h w t i r
   INSP094-CP1 →

61 agtatattcc attctggttt ttactggggg aaaggatggt gccacaagat gtcagtccat
   s i f h s g f y w g k g c c h k m s v h

121 ttattcattc atatatccaa tagatatattt atgaccactt ccatgtgccg ggagatggct
   l f i h i s n r y f m t t s m c q e m a

181 aagatccttg gaagacagat aaaatgctac ctaccaactc aaagtccagt tagggagtca
   k i l g r q i k c y l p t q s p v r e s

241 gggggtaaaa caatattcta gcaca
   g g k t i f
   ← INSP094-CP2

```

Position and sense of PCR primers →

Figure 7: Map of pCR4-TOPO-INSP094

Molecule: pCR4-TOPO-INSP094, 4222 bps DNA Circular

Type	Start	End	Name	Description
REGION	205	221	M13R	M13 rev priming site
REGION	243	262	T3	T3 priming site
MARKER	316		C CP2	INSP094-CP2
REGION	559	295	C Insert	Inserted INSP094-F2R2 PCR product
GENE	559	299	C cds?	INSP094-F2R2 cds?
MARKER	559		C CP1	INSP094-CP1
REGION	593	612	T7	T7 priming site
REGION	620	635	M13F	M13 for priming site
GENE	1424	2218	Kan	Kanamycin resistance gene ORF
GENE	2422	3282	Amp	Ampicillin resistance gene ORF
REGION	3427	4100	pUC ori	pUC origin

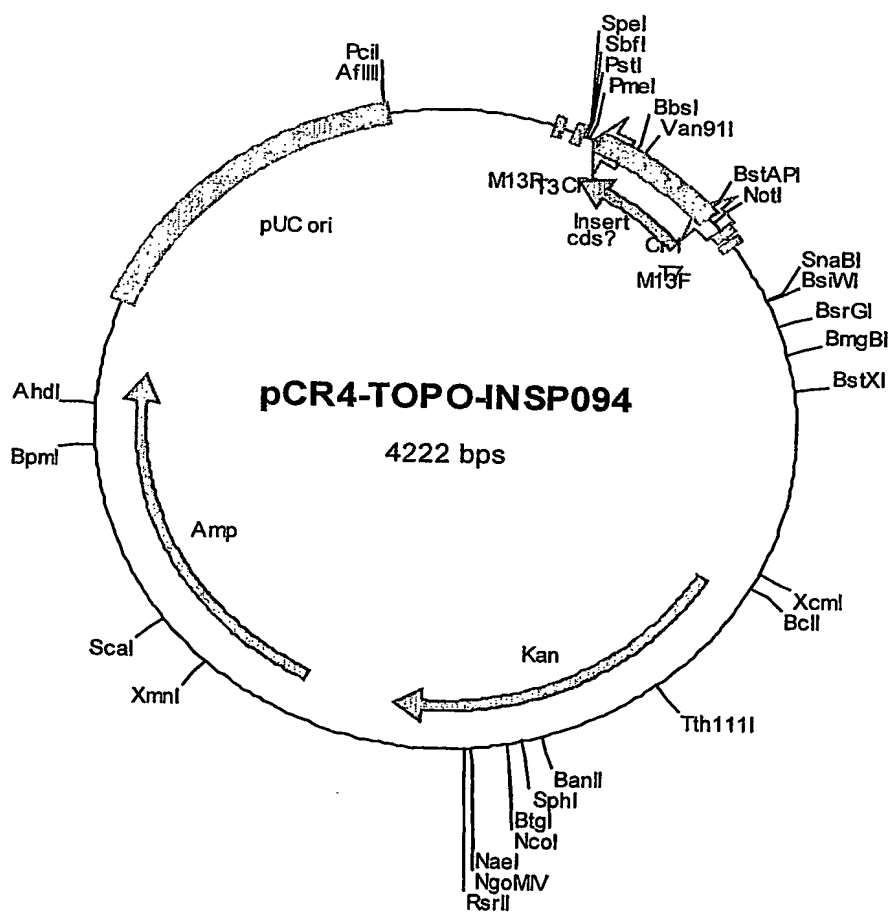


Figure 8: Map of pDONR 221

Molecule: pDONR221, 4759 bps DNA Circular
 File Name: pDONR221.cm5

Description:

Type	Start	End	Name	Description
REGION	295	268	C rrnB T2	transcription termination sequence
REGION	470	427	C rrnB T1	
REGION	536	553	21M13	transcription termination sequence
REGION	570	801	attP1	M13 Forward primer
GENE	1197	1502	ccdB	Chloramphenicol resistance gene
GENE	1844	2503	Cm r	
REGION	2751	2982	attP2	M13 Reverse primer
REGION	3040	3023	C M13 Rev	
GENE	3153	3962	Kan r	
REGION	4083	4756	pUC ori	

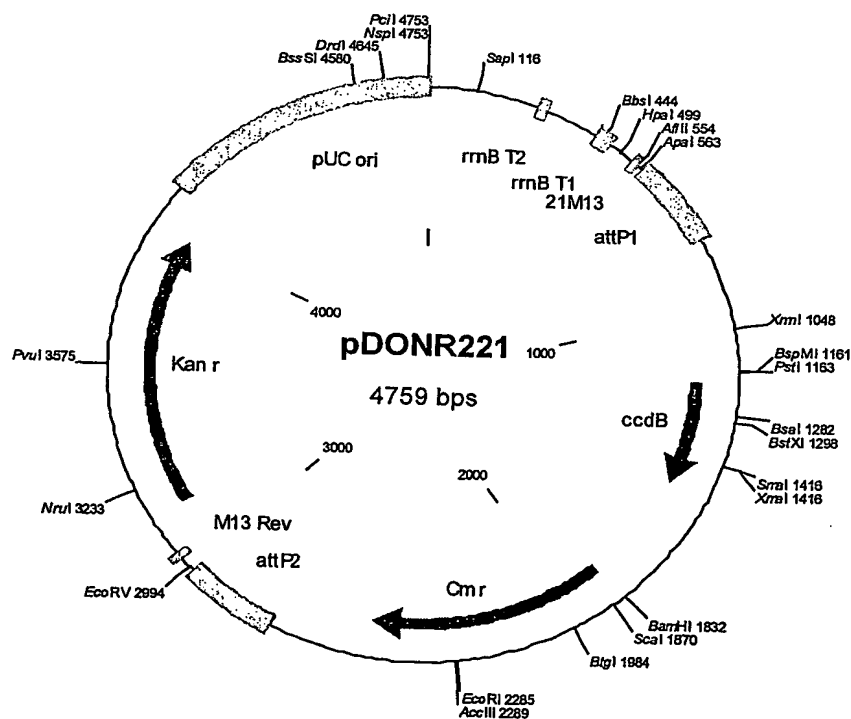


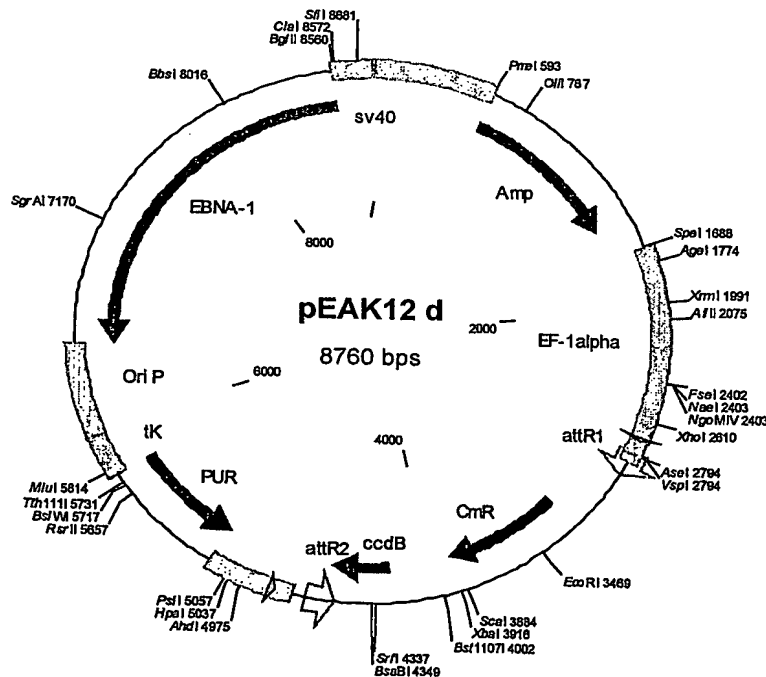
Figure 9: Map of expression vector pEAK12d

Molecule: pEAK12 d, 8760 bps DNA Circular
 File Name: pEAK12DEST.cm5

Description: Mammalian cell expression vector (plasmid ID 11345)

Molecule Features:

Type	Start	End	Name	Description
REGION	2	595		pmb-ori
GENE	596	1519	Amp	
REGION	1690	2795	EF-1alpha	
REGION	2703	2722		position of pEAK12F primer
REGION	2796	2845		MCS
MARKER	2855		attR1	
GENE	3256	3915	CmR	
GENE	4257	4562	ccdB	
MARKER	4603		C attR2	
REGION	4733	4733		MCS
REGION	4734	5162		poly A/splice
REGION	4819	4848	C	position of pEAK12R primer
GENE	5781	5163	C PUR	PUROMYCIN
REGION	6005	5782	C tK	tK promoter
REGION	6500	6006	C Ori P	
GENE	8552	6500	C EBNA-1	
REGION	8553	8752	sv40	



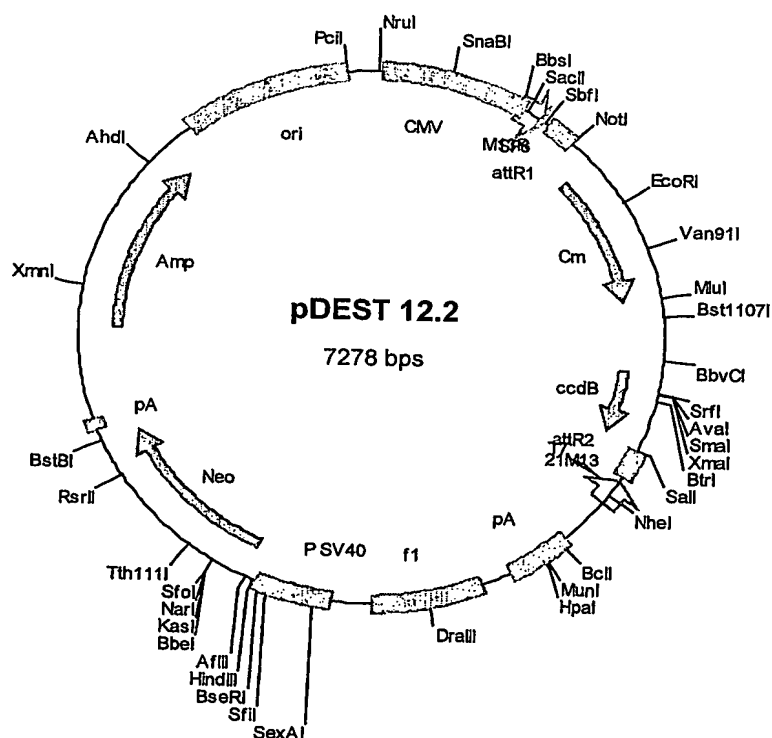
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Figure 10: Map of expression vector pDEST12.2

Molecule: pDEST 12.2, 7278 bps DNA Circular
File Name: pDEST12-2.cm5

Description: Eukaryotic expression vector

Type	Start	End	Name	Description
REGION	15	608	CMV	CMV promoter
MARKER	648		M13R	M13R primer
REGION	687	706	SP6	SP6 promoter
REGION	730	854	attR1	
GENE	963	1622	Cm	
GENE	1964	2269	ccdB	
REGION	2310	2434	attR2	
GENE	2484	2464	C T7	T7 promoter
MARKER	2512		C 21M13	21M13 primer
REGION	2784	3050	pA	SV40 polyadenylation signal
REGION	3176	3631	f1	f1 intergenic region
REGION	3791	4099	P SV40	SV40 ori & early promoter
GENE	4158	4952	Neo	
REGION	5016	5064	pA	synthetic poly adenylation signal
GENE	5475	6335	Amp	
REGION	6480	7153	ori	pUC ori

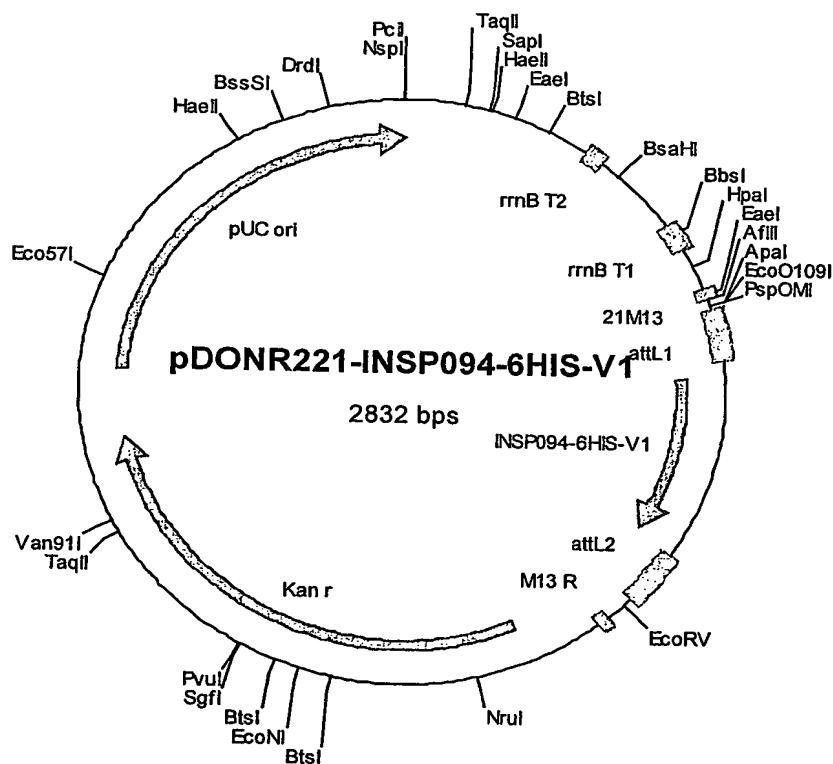


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Figure 11: Map of pENTR-INSP094-6HIS

Molecule: pDONR221-INSP094-6HIS-V1, 2832 bps DNA Circular
 File Name: pDONR221-INSP094-6HIS-V1.cm5

Type	Start	End	Name	Description
REGION	295	268	C rrnB T2	transcription termination sequence
REGION	470	427	C rrnB T1	transcription termination sequence
REGION	536	553	21M13	21M13 primer
REGION	570	651	attL1	
GENE	677	952	INSP094-6HIS-V1	
REGION	967	1055	attL2	
REGION	1113	1096	C M13 R	M13R primer
GENE	1226	2035	Kan r	
GENE	2156	2829	pUC ori	



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Figure 12: Map of pEAK12d-INSP094-6HIS

Molecule: pEAK12d-INSP094-6HIS-V1, 7225 bps DNA Circular
 File Name: pEAK12d-INSP094-6HIS-V1.cm5

Type	Start	End	Name	Description
REGION	2	595	pmb-ori	
GENE	596	1519	Amp	
REGION	1690	2795	EF-1alpha	
REGION	2703	2722	peak12-F	forward primer
REGION	2855	2874	attB1	
GENE	2888	3163	INSP094-6HIS-V1	
REGION	3171	3192	attB2	
REGION	3199	3627	'A	poly A/splice
REGION	3313	3294	C peak12-R	reverse primer
GENE	4246	3628	C PUR	PUROMYCIN
REGION	4470	4247	C tK	tK promoter
REGION	4965	4471	C Ori P	
GENE	7017	4965	C EBNA-1	
REGION	7018	7217	sv40	

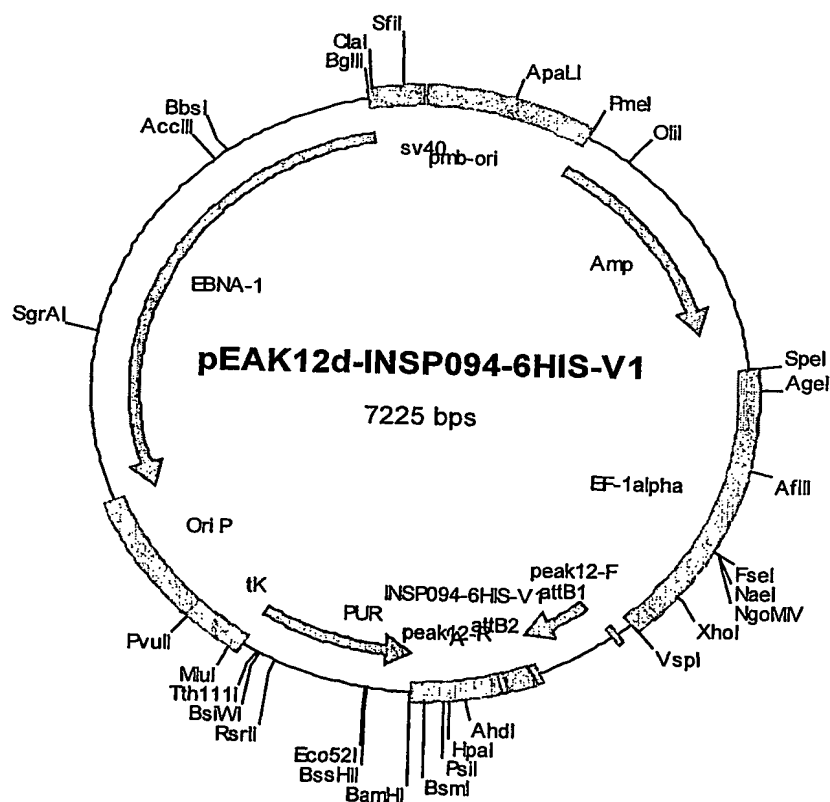


Figure 13: Map of pDEST12.2-INSP094-6HIS

Molecule: pDEST12.2-INSP094-6HIS-V1, 5911 bps DNA Circular
 File Name: pDEST12.2-INSP094-6HIS-V1.cm5

Type	Start	End	Name	Description
GENE	15	537	CMV promoter	
REGION	648	665	M13rev	M13R primer
REGION	687	704	SP6	SP6 primer
REGION	730	762	attB1	
GENE	763	1038	INSP094-6HIS-V1	
REGION	1042	1067	attB2	
REGION	1117	1097	C T7	T7 promoter
REGION	1146	1128	C 21M13	21M13 primer
GENE	1252	1614	pA	SV40 polyadenylation signal
GENE	1808	2264	f1	f1 intergenic region
GENE	2328	2746	P SV40	SV40 ori & early promoter
GENE	2791	3585	Neo	
GENE	3649	3697	pA	poly adenylation signal
GENE	4108	4968	Amp	
GENE	5117	5756	ori	pUC ori

